What is claimed is:

1.

A genomic cloning method for identifying DNA segments containing genes in complex genomes, said method comprising:

constructing a genomic library in an environment that eliminates repetitive sequences, said library comprising fragments of genomic DNA;

inserting said genomic DNA into a suitable vector, and characterizing said DNA segment.

2.

The method of claim 1 further comprising the step of randomly shearing said genomic DNA for insertion into said vector.

3.

The method of claim 1 further comprising the steps of size fractionating said genomic DNA.

4.

The method of claim 1 wherein the restrictive environment is established using mechanical size fractionation of said DNA and selective hybridization followed by hydroxylapatite chromatography.

5.

The method of claim 1 wherein said hydroxylapitite selective hybridization is conducted at Cot values between 0.01 and 100.

6.

The method of claim 1 wherein the size fractionated DNA fragments are fragments of a size smaller than the size of uninterrupted genetic sequences in the genomic DNA.

7.

The method of claim 1 wherein the size fractionated DNA fragments range from about 0.5 to about 4 kilobase pairs.

8.

The method of claim 1 wherein said vector is selected from a group consisting of: phage, plasmid or other suitable vectors.

9.

The method of claim 1 wherein said phage vector is M13.

10.

The method of claim 1 wherein said complex genome is a plant genome.

11.

The method of claim 1 where said genome is a cereal grain genome.

12.

The method of claim 8 wherein said plant genome is selected from the group consisting of: maize, rice, Brassica, soybean, and wheat.

13.

The method of claim 1 wherein said complex genome is a mammalian genome.

14.

A genomic cloning method for identifying DNA segments containing genes in complex genomes, said method comprising:

constructing a genomic library in an environment that eliminates repetitive sequences, said library comprising fragments of genomic DNA;

said environment established using mechanical shearing of said genomic DNA, selective hybridization at Cot values of between approximately 0.01 and 100, followed by hydroxylapatite chromatography;

inserting said genomic DNA into a suitable vector, and characterizing said DNA segment.

15.

A genomic cloning method for identifying DNA segments containing genes in complex genomes, said method comprising:

constructing a genomic library in a methylation restrictive environment, said library comprising fragments of genomic DNA;

inserting said genomic DNA into a suitable vector, and characterizing said DNA segment.

16.

The method of claim 15 further comprising the step of randomly shearing said genomic DNA for insertion into said vector.

17.

The method of claim 15 further comprising the steps of size fractionating said genomic DNA.

18.

The method of claim 15 wherein the methylation restrictive environment comprises cell extracts of methylation restrictive bacteria: $mcrA^+/mcrBC^+$, $mcrA^-/mcrBC^+$ or $mcrA^+/mcrBC^-$, or any other methylation restriction system that has similar properties to the mcr system.

19.

The method of claim 18 wherein said methylation restrictive bacterial strain is selected from a group comprising: JM101, JM107, and JM109.

20.

The method of claim 15 wherein the methylation restrictive environment comprises cell-free enzyme encoded by a methylation restrictive bacterial gene: $mcrA^+/mcrBC^+$, $mcrA^-/mcrBC^+$ or $mcrA^+/mcrBC^-$, or any other methylation restriction system that has similar properties to the mcr system.

21.

The method of claim 15 wherein the methylation restrictive environment comprises cell-free enzyme encoded by mcrBC.

22.

The method of claim 15 wherein the size fractionated DNA fragments are fragments of a size smaller than the size of uninterrupted genetic sequences in the genomic DNA.

23.

The method of claim 15 wherein the size fractionated DNA fragments range from about 0.5 to about 4 kilobase pairs and the DNA is cleaved with a methylation insensitive restriction enzyme.

24.

The method of claim 15 wherein a methylation insensitive endonuclease is employed to generate DNA fragments.

25.

The method of claim 23 wherein said methylation insensitive endonuclease is *Spe* I.

26.

The method of claim 15 wherein said vector is selected from a group consisting of: phage, plasmid or other suitable vectors.

27.

The method of claim 15 wherein said phage vector is M13.

28.

The method of claim 15 wherein said complex genome is a plant genome.

29.

The method of claim 15 where said genome is a cereal grain genome.

30.

The method of claim 28 wherein said plant genome is selected from the group consisting of: maize, rice, Brassica, soybean, and wheat.

31.

The method of claim 15 wherein said complex genome is a mammalian genome.

32.

A genomic cloning method for identifying DNA segments containing genes in complex genomes, said method comprising:

constructing a genomic library in an environment that eliminates repetitive sequences by selective protein binding of said genomic DNA, said library comprising fragments of genomic DNA;

inserting said genomic DNA into a suitable vector, and characterizing said DNA segment.

33.

The method of claim 32 further comprising the step of randomly shearing said genomic DNA for insertion into said vector.

34.

The method of claim 32 further comprising the steps of size fractionating said genomic DNA.

35.

The method of claim 32 wherein the restrictive environment is established using mechanical size fractionation of said DNA and by methyl-CpG binding domain protein chromatography.

36.

The method of claim 32 wherein the size fractionated DNA fragments are fragments of a size smaller than the size of uninterrupted genetic sequences in the genomic DNA.

37.

The method of claim 32 wherein the size fractionated DNA fragments range from about 0.5 to about 4 kilobase pairs.

38.

The method of claim 32 wherein said vector is selected from a group consisting of: phage, plasmid or other suitable vectors.

39.

The method of claim 32 wherein said phage vector is M13.

40.

The method of claim 32 wherein said complex genome is a plant genome.

41.

The method of claim 32 where said genome is a cereal grain genome.

42.

The method of claim 40 wherein said plant genome is selected from the group consisting of: maize, rice, Brassica, soybean, and wheat.

43.

The method of claim 40 wherein said complex genome is a mammalian genome.

44.

The method of claim 32 wherein said column chromatography is conducted using an elution buffer of approximately 0.4 M NaCl.

45.

The method of claim 32 wherein said column chromatography is conducted using Ni2+ NTA agarose.